SCREENING OF USEFUL SNP MARKERS FOR MISSING CHILDREN IDENTIFICATION IN KOREA

<u>Moon-hee Park</u>¹, Eung-Soo Kim¹, Eun-Young Cho⁴, Jong-Eun Lee⁴, Hyn-Jun Kang³, Ha-Chin Sung³, Myunsoo Han² and Seung-beom Hong^{1, 3}

¹Eastern District Office, National Institute of Scientific Investigation, DNA Analysis Section, Wonju-Si, Gwangwon-Do, Republic of Korea

²DNA Identification Center, National Institute of Scientific Investigation, Seoul, Republic of Korea

³School of Life Science and Biotechnology, Korea University, Seoul, Republic of Korea

⁴DNA LINK. Inc., Seoul, Republic of Korea

Korean DNA database law for missing children identification has been in effect since 2005, and the number of missing persons exceeds over 20,000 by now. For gross kinship database searching, we have encountered the low exclusion chance and the mutation problem.

To overcome these problems, we screened the informative SNP markers with a same PCR condition, tested the linkage disequilibrium with the conventional STR markers, and finally selected the 35 SNP markers. The estimation of the allele frequencies and the exact test for the 35 SNP markers and 17 conventional STR markers show the Hardy–Weinberg equilibrium (P > 0.05) and independent inheritance. These 35 SNPs are expected to provide an additional useful discrimination power for the missing children DNA database.